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Inventors:

Hollingsworth et al.

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## Amendments to the Specification:

Please replace the paragraph beginning at page 28, line 16, with the following rewritten paragraph:

--Two web-based algorithms were used to analyze the amino acid sequence of MUC1 cytoplasmic tail for potential human and murine MHC class I and class II binding epitopes. The first algorithm, "SYFPEITHI," (Rammensee, et al (1999) supra) was available at <a href="http://www.uni-tuebingen.de/uni/kxi/">http://www.uni-tuebingen.de/uni/kxi/</a>. This algorithm ranks peptides according to a score taking into account the presence of primary and secondary MHC-binding anchor residues. The second algorithm, "BIMAS," (Parker, et al (1994) supra) was available at <a href="http://bimas.dert.nih.gov/molbio/hla bind/">http://bimas.dert.nih.gov/molbio/hla bind/</a>. This algorithm ranks potential binding according to the predicted half-time of dissociation of peptide/MHC complexes.--